

1642

CRF1P#25

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USPTO
SEARCH CENTER 1600/2000
1600

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/558,741

DATE: 06/18/2002

TIME: 07:58:57

Input Set : N:\Crf3\Datahold\EFS\09558741\CIBT-P01-130SequenceListing.txt
Output Set: N:\CRF3\06182002\I558741.raw

5 <110> APPLICANT: Huston, J.
 6 Houston, L.L.
 7 Ring, D.
 8 Oppermann, H.
 10 <120> TITLE OF INVENTION: BIOSYNTHETIC BINDING PROTEINS FOR IMMUNO-TARGETING
 12 <130> FILE REFERENCE: CIBT-P01-130
 14 <140> CURRENT APPLICATION NUMBER: 09/558,741
 15 <141> CURRENT FILING DATE: 2000-04-26
 17 <150> PRIOR APPLICATION NUMBER: 07/831,967
 18 <151> PRIOR FILING DATE: 1992-02-06
 20 <160> NUMBER OF SEQ ID NOS: 16
 22 <170> SOFTWARE: PatentIn version 3.1
 24 <210> SEQ ID NO: 1
 25 <211> LENGTH: 909
 26 <212> TYPE: DNA
 27 <213> ORGANISM: Artificial Sequence
 29 <220> FEATURE:
 30 <223> OTHER INFORMATION: 741F8 sfv'
 32 <220> FEATURE:
 33 <221> NAME/KEY: CDS
 34 <222> LOCATION: (3)..(752)
 35 <223> OTHER INFORMATION:
 37 <400> SEQUENCE: 1
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 40 1 5 10 15
 42 cct gga gag aca gtc aag atc tcc tgc aag gct tot ggg tat acc ttc 95
 43 Pro Gly Glu Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe
 44 20 25 30
 46 aca aac tat gga atg aac tgg gtg aag cag gct cca gga aag ggt tta 143
 47 Thr Asn Tyr Gly Met Asn Trp Val Lys Gln Ala Pro Gly Lys Gly Leu
 48 35 40 45
 50 aag tgg atg ggc tgg ata aac acc aac act gga gag cca aca tat gct 191
 51 Lys Trp Met Gly Trp Ile Asn Thr Asn Thr Gly Glu Pro Thr Tyr Ala
 52 50 55 60
 54 gaa gag ttc aag gga cgg ttt gcc ttc tct ttg gaa acc tct gcc agc 239
 55 Glu Glu Phe Lys Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser
 56 65 70 75
 58 act gcc tat ttg cag atc aag aag ctc aaa aat gag gac acg gct aca 287
 59 Thr Ala Tyr Leu Gln Ile Lys Lys Leu Lys Asn Glu Asp Thr Ala Thr
 60 80 85 90 95
 63 tat ttc tgt gga agg caa ttt att acc tac ggc ggg ttt gct aac tgg 335
 64 Tyr Phe Cys Gly Arg Gln Phe Ile Thr Tyr Gly Gly Phe Ala Asn Trp

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65	100	105	110	
67	ggc caa ggg act ctg gtc act gtc tct gca tcg agc tcc tcc gga tct			383
68	Gly Gln Gly Thr Leu Val Thr Val Ser Ala Ser Ser Ser Ser Gly Ser			
69	115	120	125	
71	tca tct agc ggt tcc agc tcg agc gat atc gtc atg acc cag tct cct			431
72	Ser Ser Ser Gly Ser Ser Ser Asp Ile Val Met Thr Gln Ser Pro			
73	130	135	140	
75	aaa ttc atg tcc acg tca gtg gga gac agg gtc agc atc tcc tgc aag			479
76	Lys Phe Met Ser Thr Ser Val Gly Asp Arg Val Ser Ile Ser Cys Lys			
77	145	150	155	
79	gcc agt cag gat gtg agt act gct gta gcc tgg tat caa caa aaa cca			527
80	Ala Ser Gln Asp Val Ser Thr Ala Val Ala Trp Tyr Gln Gln Lys Pro			
81	160	165	170	175
83	ggg caa tct cct aaa cta ctg att tac tgg aca tcc acc cgg cac act			575
84	Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp Thr Ser Thr Arg His Thr			
85	180	185	190	
87	gga gtc cct gat cgc ttc aca ggc agt gga tct ggg aca gat tat act			623
88	Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Tyr Thr			
89	195	200	205	
91	ctc acc atc agc agt gtg cag gct gaa gac ctg gca ctt cat tac tgt			671
92	Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Leu His Tyr Cys			
93	210	215	220	
95	cag caa cat tat aga gtg ccg tac acg ttc gga ggg ggg acc aag ctg			719
96	Gln Gln His Tyr Arg Val Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu			
97	225	230	235	
99	gag ata aaa cgg gct gat ggg gga ggt gga tgt taacggggga ggtggatgtt			772
100	Glu Ile Lys Arg Ala Asp Gly Gly Gly Cys			
101	240	245	250	
103	gggtctcggtt acgttgcgga tctcgaggct atctttacta actcttaccc taaagttctg			832
105	gctcaactgt ctgcacgcaa gctttgcag gatatcatga gcgcttaaga tccgtcgacc			892
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112	<212> TYPE: PRT			
113	<213> ORGANISM: Artificial Sequence			
115	<220> FEATURE:			
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126	20	25	30	
129	Asn Tyr Gly Met Asn Trp Val Lys Gln Ala Pro Gly Lys Gly Leu Lys			
130	35	40	45	
133	Trp Met Gly Trp Ile Asn Thr Asn Thr Gly Glu Pro Thr Tyr Ala Glu			
134	50	55	60	
137	Glu Phe Lys Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser Thr			
138	65	70	75	80
141	Ala Tyr Leu Gln Ile Lys Lys Leu Lys Asn Glu Asp Thr Ala Thr Tyr			

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Input Set : N:\Crf3\Datohold\EFS\09558741\CIIBT-P01-130SequenceListing.txt
Output Set: N:\CRF3\06182002\I558741.raw

142 85 90 95
145 Phe Cys Gly Arg Gln Phe Ile Thr Tyr Gly Gly Phe Ala Asn Trp Gly
146 100 105 110
149 Gln Gly Thr Leu Val Thr Val Ser Ala Ser Ser Ser Ser Gly Ser Ser
150 115 120 125
153 Ser Ser Gly Ser Ser Ser Asp Ile Val Met Thr Gln Ser Pro Lys
154 130 135 140
157 Phe Met Ser Thr Ser Val Gly Asp Arg Val Ser Ile Ser Cys Lys Ala
158 145 150 155 160
161 Ser Gln Asp Val Ser Thr Ala Val Ala Trp Tyr Gln Gln Lys Pro Gly
162 165 170 175
165 Gln Ser Pro Lys Leu Leu Ile Tyr Trp Thr Ser Thr Arg His Thr Gly
166 180 185 190
169 Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu
170 195 200 205
173 Thr Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Leu His Tyr Cys Gln
174 210 215 220
177 Gln His Tyr Arg Val Pro Tyr Thr Phe Gly Gly Thr Lys Leu Glu
178 225 230 235 240
181 Ile Lys Arg Ala Asp Gly Gly Gly Cys
182 245 250
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186 <211> LENGTH: 779
187 <212> TYPE: DNA
188 <213> ORGANISM: Artificial Sequence
190 <220> FEATURE:
191 <223> OTHER INFORMATION: 26-10 sFv'

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193 <221> NAME/KEY: CDS
194 <222> LOCATION: (3)..(758)
195 <223> OTHER INFORMATION:
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201 1 5 10 15
203 ggc gcc tct gtg cgc atg tcc tgc aaa tcc tct ggg tac att ttc acc 95
204 Gly Ala Ser Val Arg Met Ser Cys Lys Ser Ser Gly Tyr Ile Phe Thr
205 20 25 30
207 gac ttc tac atg aat tgg gtt cgc cag tct cat ggt aag tct cta gac 143
208 Asp Phe Tyr Met Asn Trp Val Arg Gln Ser His Gly Lys Ser Leu Asp
209 35 40 45
211 tac atc ggg tac att tcc cca tac tct ggg gtt acc ggc tac aac cag 191
212 Tyr Ile Gly Tyr Ile Ser Pro Tyr Ser Gly Val Thr Gly Tyr Asn Gln
213 50 55 60
215 aag ttt aaa ggt aag gcg acc ctt act gtc gac aaa tct tcc tca act 239
216 Lys Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr
217 65 70 75
219 gct tac atg gag ctg cgt tct ttg acc tct gag gac tcc gcg gta tac 287
220 Ala Tyr Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr

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221	80	85	90	95													
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224	Tyr	Cys	Ala	Gly	Ser	Ser	Gly	Asn	Lys	Trp	Ala	Met	Asp	Tyr	Trp	Gly	
225					100				105					110			
227	cat	ggt	gtc	agt	gtt	act	gtg	agc	tcc	tcc	gga	tct	tca	tct	agc	ggt	383
228	His	Gly	Ala	Ser	Val	Thr	Val	Ser	Ser	Ser	Gly	Ser	Ser	Ser	Ser	Gly	
229						115			120					125			
231	tcc	agc	tcg	agt	gga	tcc	gac	gto	gta	atg	acc	cag	act	ccg	ctg	tct	431
232	Ser	Ser	Ser	Gly	Ser	Asp	Val	Val	Met	Thr	Gln	Thr	Pro	Leu	Ser		
233						130			135			140					
235	ctg	ccg	gtt	tct	ctg	ggt	gac	cag	gct	tct	att	tct	tgc	cgc	tct	tcc	479
236	Leu	Pro	Val	Ser	Leu	Gly	Asp	Gln	Ala	Ser	Ile	Ser	Cys	Arg	Ser	Ser	
237							145		150			155					
239	cag	tct	ctg	gtc	cat	tct	aat	ggt	aac	act	tac	ctg	aac	tgg	tac	ctg	527
240	Gln	Ser	Leu	Val	His	Ser	Asn	Gly	Asn	Thr	Tyr	Leu	Asn	Trp	Tyr	Leu	
241						160		165			170			175			
243	caa	aag	gct	ggt	cag	tct	ccg	aag	ctt	ctg	atc	tac	aaa	gtc	tct	aac	575
244	Gln	Lys	Ala	Gly	Gln	Ser	Pro	Lys	Leu	Ile	Tyr	Lys	Val	Ser	Asn		
245							180		185			190					
247	cgc	tcc	tct	ggt	gtc	ccg	gat	cgt	tcc	tct	ggt	tct	ggt	tct	ggt	act	623
248	Arg	Phe	Ser	Gly	Val	Pro	Asp	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	
249							195		200			205					
251	gac	ttc	acc	ctg	aag	atc	tct	cgt	gtc	cag	gcc	gaa	gac	ctg	ggt	atc	671
252	Asp	Phe	Thr	Leu	Lys	Ile	Ser	Arg	Val	Gln	Ala	Glu	Asp	Leu	Gly	Ile	
253						210		215			220						
255	tac	ttc	tgc	tct	cag	act	act	cat	gta	ccg	ccg	act	ttt	ggt	ggt	ggc	719
256	Tyr	Phe	Cys	Ser	Gln	Thr	Thr	His	Val	Pro	Pro	Thr	Phe	Gly	Gly		
257							225		230			235					
259	acc	aag	ctc	gag	att	aaa	cgt	tcc	ggg	gga	ggt	gga	tgt	taactgcagc		768	
260	Thr	Lys	Leu	Glu	Ile	Lys	Arg	Ser	Gly	Gly	Gly	Gly	Cys				
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277	1				5				10					15			
280	Ala	Ser	Val	Arg	Met	Ser	Cys	Lys	Ser	Ser	Gly	Tyr	Ile	Phe	Thr	Asp	
281						20			25					30			
284	Phe	Tyr	Met	Asn	Trp	Val	Arg	Gln	Ser	His	Gly	Lys	Ser	Leu	Asp	Tyr	
285							35		40			45					
288	Ile	Gly	Tyr	Ile	Ser	Pro	Tyr	Ser	Gly	Val	Thr	Gly	Tyr	Asn	Gln	Lys	
289							50		55			60					
292	Phe	Lys	Gly	Lys	Ala	Thr	Leu	Thr	Val	Asp	Lys	Ser	Ser	Ser	Thr	Ala	
293							65		70			75			80		

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296 Tyr Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr
297 85 90 95
300 Cys Ala Gly Ser Ser Gly Asn Lys Trp Ala Met Asp Tyr Trp Gly His
301 100 105 110
304 Gly Ala Ser Val Thr Val Ser Ser Gly Ser Ser Ser Gly Ser
305 115 120 125
308 Ser Ser Ser Gly Ser Asp Val Val Met Thr Gln Thr Pro Leu Ser Leu
309 130 135 140
312 Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln
313 145 150 155 160
316 Ser Leu Val His Ser Asn Gly Asn Thr Tyr Leu Asn Trp Tyr Leu Gln
317 165 170 175
320 Lys Ala Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg
321 180 185 190
324 Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
325 195 200 205
328 Phe Thr Leu Lys Ile Ser Arg Val Gln Ala Glu Asp Leu Gly Ile Tyr
329 210 215 220
332 Phe Cys Ser Gln Thr Thr His Val Pro Pro Thr Phe Gly Gly Gly Thr
333 225 230 235 240
336 Lys Leu Glu Ile Lys Arg Ser Gly Gly Gly Gly Cys
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350 <222> LOCATION: (1)..(729)
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357 1 5 10 15
359 aca gtc aag atc tcc tgc aag gct tct gga tat acc ttc gca aac tat 96
360 Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ala Asn Tyr
361 20 25 30
363 gga atg aac tgg atg aag cag gct cca gga aag ggt tta aag tgg atg 144
364 Gly Met Asn Trp Met Lys Gln Ala Pro Gly Lys Gly Leu Lys Trp Met
365 35 40 45
367 ggc tgg ata aac acc tac act gga cag tca aca tat gct gat gac ttc 192
368 Gly Trp Ile Asn Thr Tyr Thr Gly Gln Ser Thr Tyr Ala Asp Asp Phe
369 50 55 60
373 aag gaa cgg ttt gcc ttc tct ttg gaa acc tct gcc acc act gcc cat 240
374 Lys Glu Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Thr Thr Ala His
375 65 70 75 80
377 ttg cag atc aac aac ctc aga aat gag gac tcg gcc aca tat ttc tgt 288

VERIFICATION SUMMARY

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Input Set : N:\Crf3\Datahold\EFS\09558741\CIBT-P01-130SequenceListing.txt
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